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FIG. 2

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*Escherichia coli*  
*Escherichia coli*

UCCUUGGCCCCGUAGGCCGAGCCACCCAUCCGAGUAGAGUACCCGUACCCGUAGGUAGGUCCGUUCCGUAGGAC  
ACUAGGAAUCCCAGGCCAU

100  
120

FIG. 3

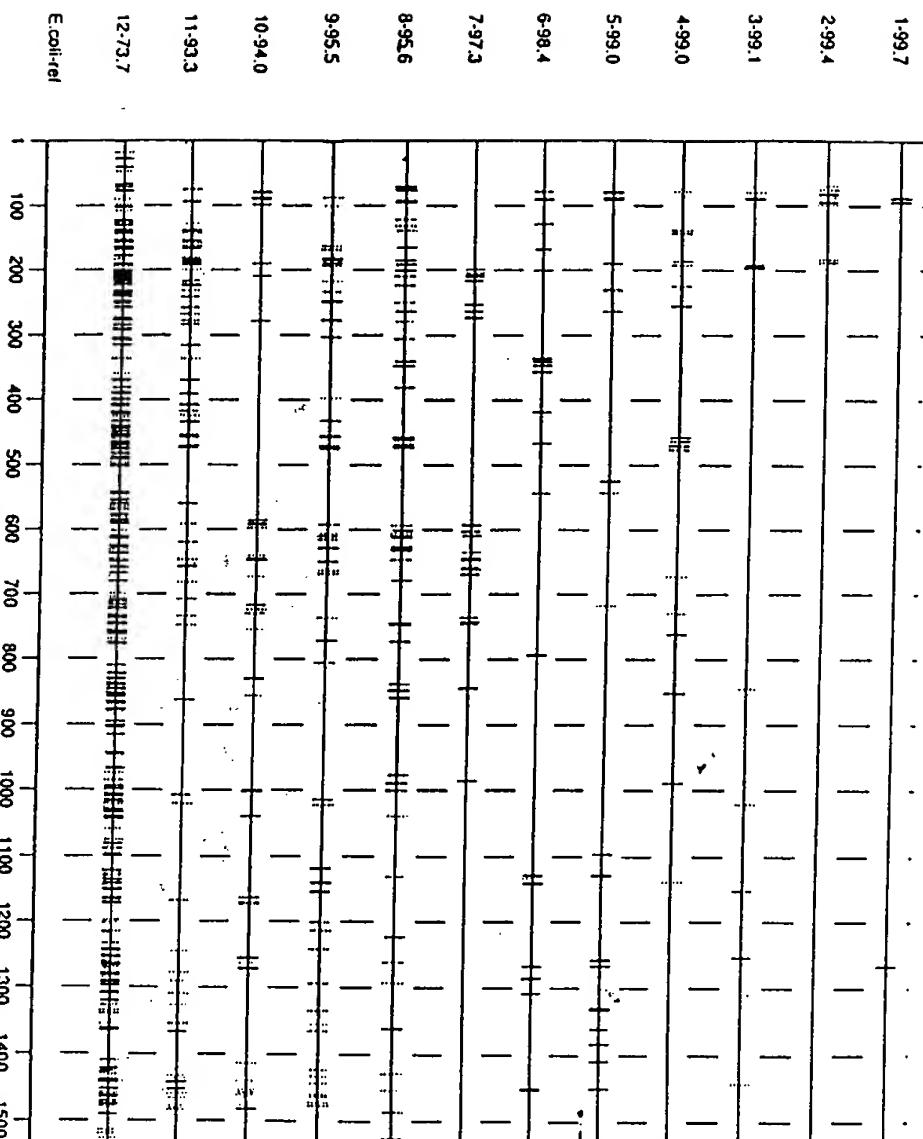
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FIG. 4

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FIG. 6

## Summary of 16S rRNA Analysis



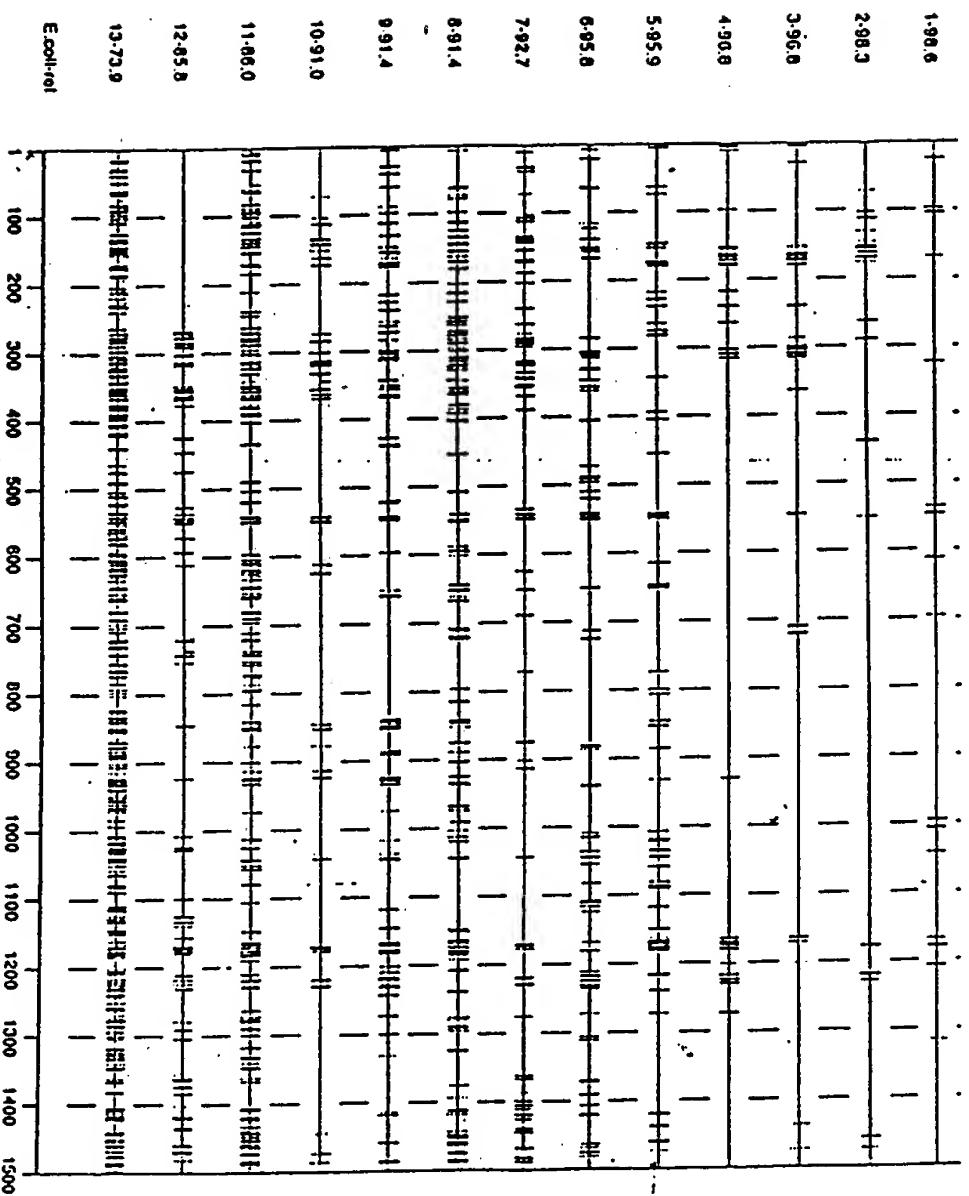
## LEGEND:

Summary of 16S rRNA Analysis (Listing of Bacteria and percent similarity included in analysis)

1. 99.7% *Clostridium botulinum* G-Clostridium subterminaliae; 2. 99.4% *Streptococcus cremoris*-*Streptococcus lactis*; 3. 99.1% *Lactobacillus lactis*-*Lactobacillus delbrueckii*; 4. 99.0% *Neisseria gonorrhoeae*-*Neisseria meningitidis*; 5. 99.0% *Mycobacterium intracellulare* *Mycobacterium avium*; 6. 98.4% *Mycobacterium avium*-*Mycobacterium tuberculosis*; 7. 97.3% *Pseudomonas alcaligenes*-*Pseudomonas stutzeri*; 8. 95.6% *Chlamydia psittaci*-*Chlamydia trachomatis*; 9. 95.5% *Spiroplasma citri*-*Spiroplasma mirum*; 10. 94.0% *Clostridium lituseburense*-*Clostridium sodelleii*; 11. 93.3% *Listeria monocytogenes*-*Bacillus thuringiensis*; 12. 73.7% *Escherichia coli*-*Bacteroides fragilis*.

## Summary of 23S rRNA Analysis

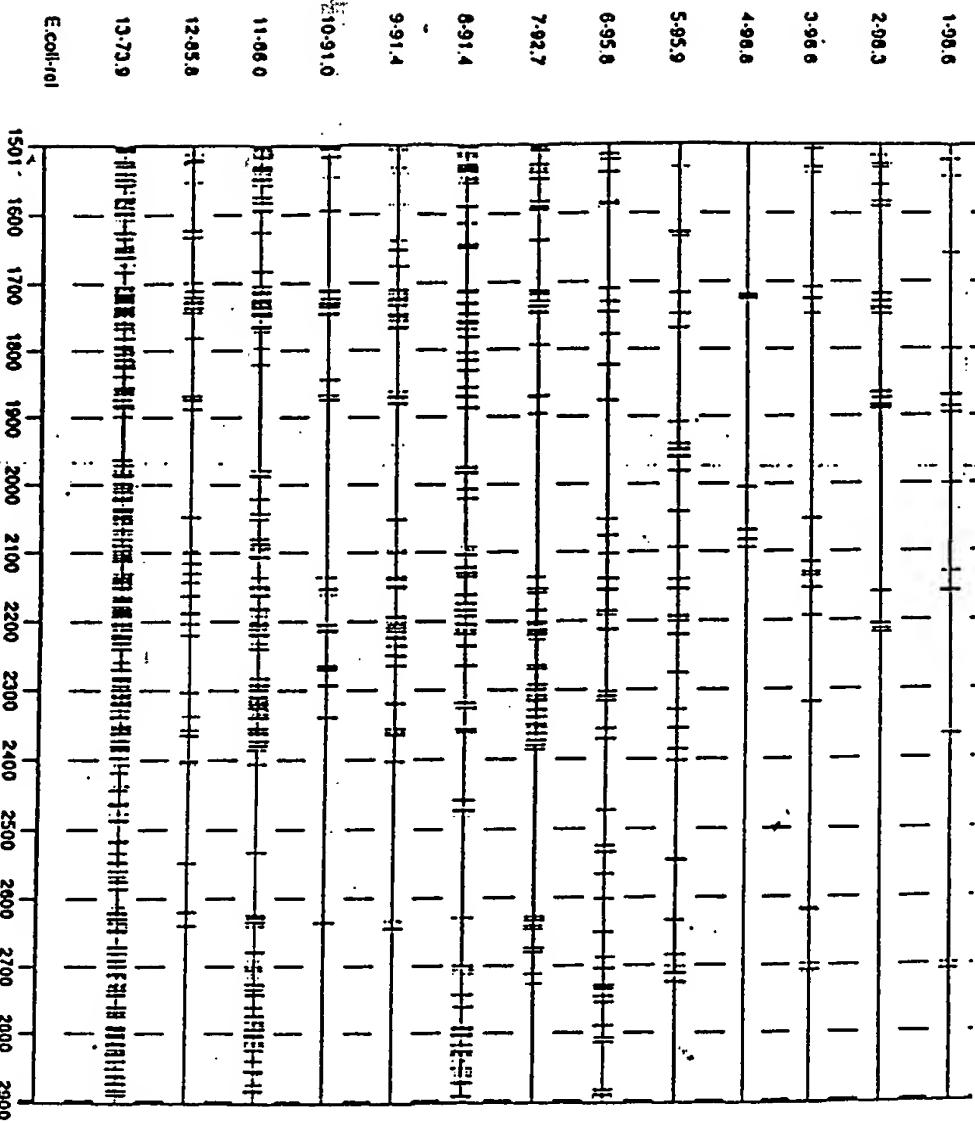
FIG. 7



LEGEND: Summary of 23S rRNA Analysis (Listing of Bacteria and percent similarity included in analysis)

1. 98.6% *Neisseria gonorrhoeae*-*Neisseria meningitidis*; 2. 98.3% *Proteus mirabilis*-*Proteus vulgaris*; 3. 96.8% *Mycobacterium intracellulare*-*Mycobacterium avium*; 4. 96.8% *Mycobacterium avium*-*Mycobacterium asiaticum*; 5. 95.9% *Mycobacterium tuberculosis*-*Mycobacterium kansasi*; 6. 95.8% *Nicotiana tabacum* (tobacco)-*Zea mays* (maize); 7. 92.7% *Proteus vulgaris*-*Klebsiella rhinoscleromatis*; 8. 91.4% *Bacillus stearothermophilus*-*Bacillus subtilis*; 9. 91.4% *Mycobacterium intracellulare*-*Mycobacterium fortuitum*; 10. 91.0% *Escherichia coli*-*Klebsiella rhinoscleromatis*; 11. 86.0% *Escherichia coli*-*pseudomonas aeruginosa*; 12. 85.8% *Escherichia coli*-*Chlamydia psittaci*; 13. 73.9% *Escherichia coli*-*Anacystis nidulans*.

## Summary of 23S rRNA Analysis



LEGEND: Summary of 23S rRNA Analysis (Listing of Bacteria and percent similarity included in analysis)

1. 98.6% *Neisseria gonorrhoeae*-*Neisseria meningitidis*; 2. 98.3% *Proteus mirabilis*-*Proteus vulgaris*; 3. 96.8% *Mycobacterium intracellulare*-*Mycobacterium avium*; 4. 96.0% *Mycobacterium avium*-*Mycobacterium asiaticum*; 5. 95.9% *Mycobacterium tuberculosis*-*Mycobacterium kansasii*; 6. 95.8% *Nicotiana tabacum* (tobacco)-*zea mays* (maize); 7. 92.7% *Proteus vulgaris*-*Klebsiella rhinoscleromatis*; 8. 91.4% *Bacillus stearothermophilus*-*Bacillus subtilis*; 9. 91.4% *Myc bacterium intracellulara*-*Mycobacterium fortuitum*; 10. 91.0% *Escherichia coli*-*Klebsiella rhinoscleromatis*; 11. 86.0% *Escherichia coli*-*Pseudomonas aeruginosa*; 12. 85.0% *Chlamydia trachomatis*-*Chlamydia psittaci*; 13. 73.9% *Escherichia coli*-*Anacystis nidulans*.

Summary of 16S rRNA PROBE locations

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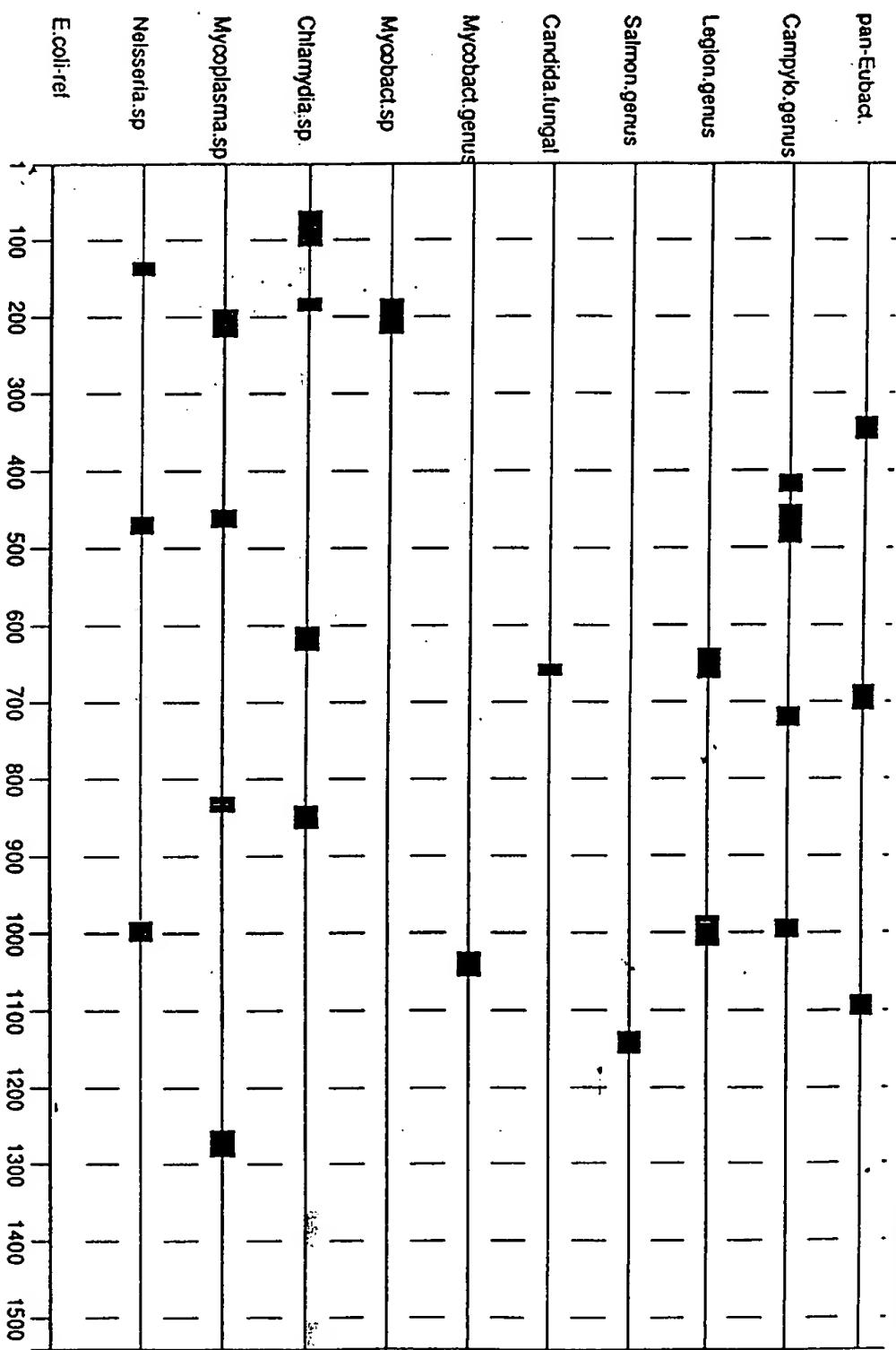


FIG. 9

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## Summary of 23S rRNA PROBE locations

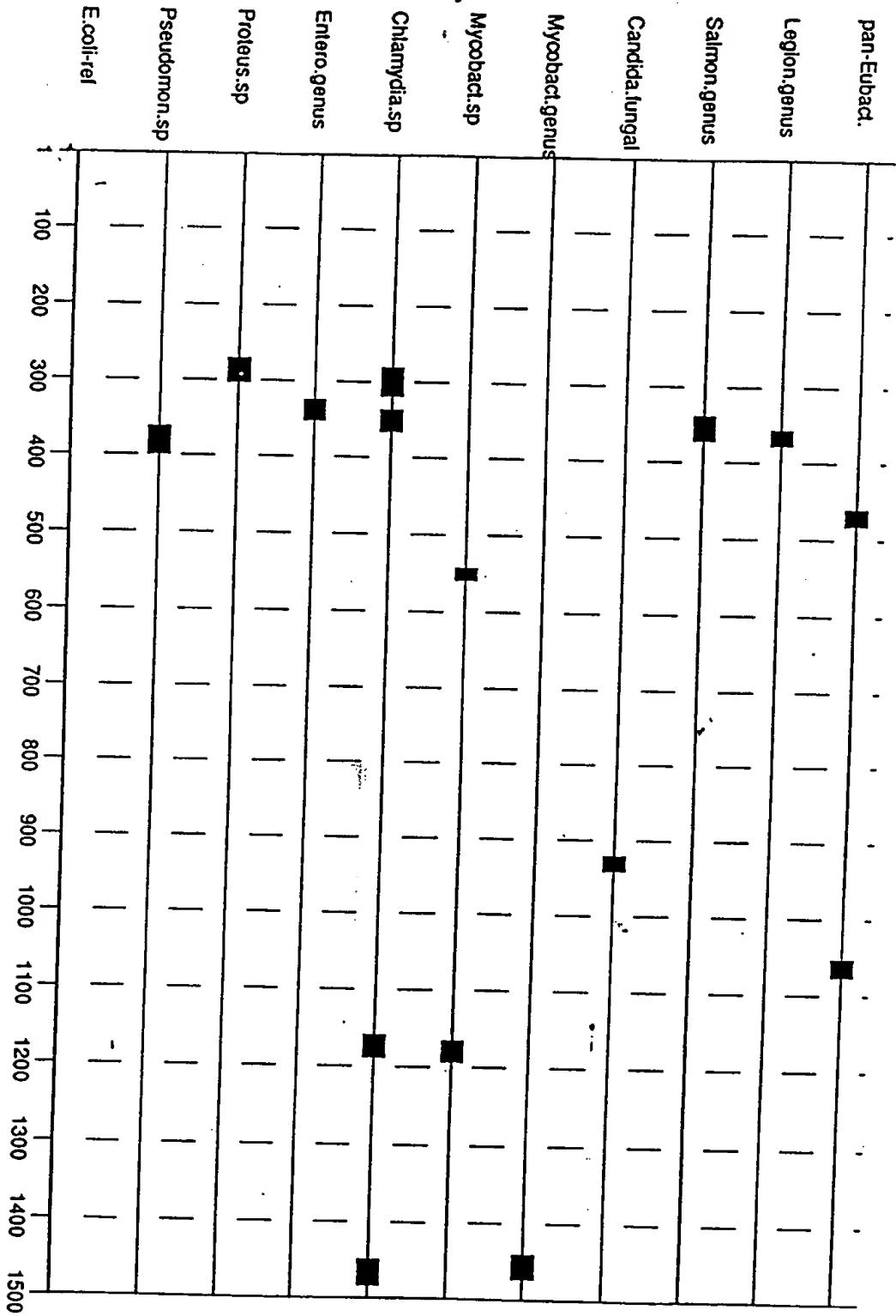


FIG. 10

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Summary of 23S rRNA PROBE locations

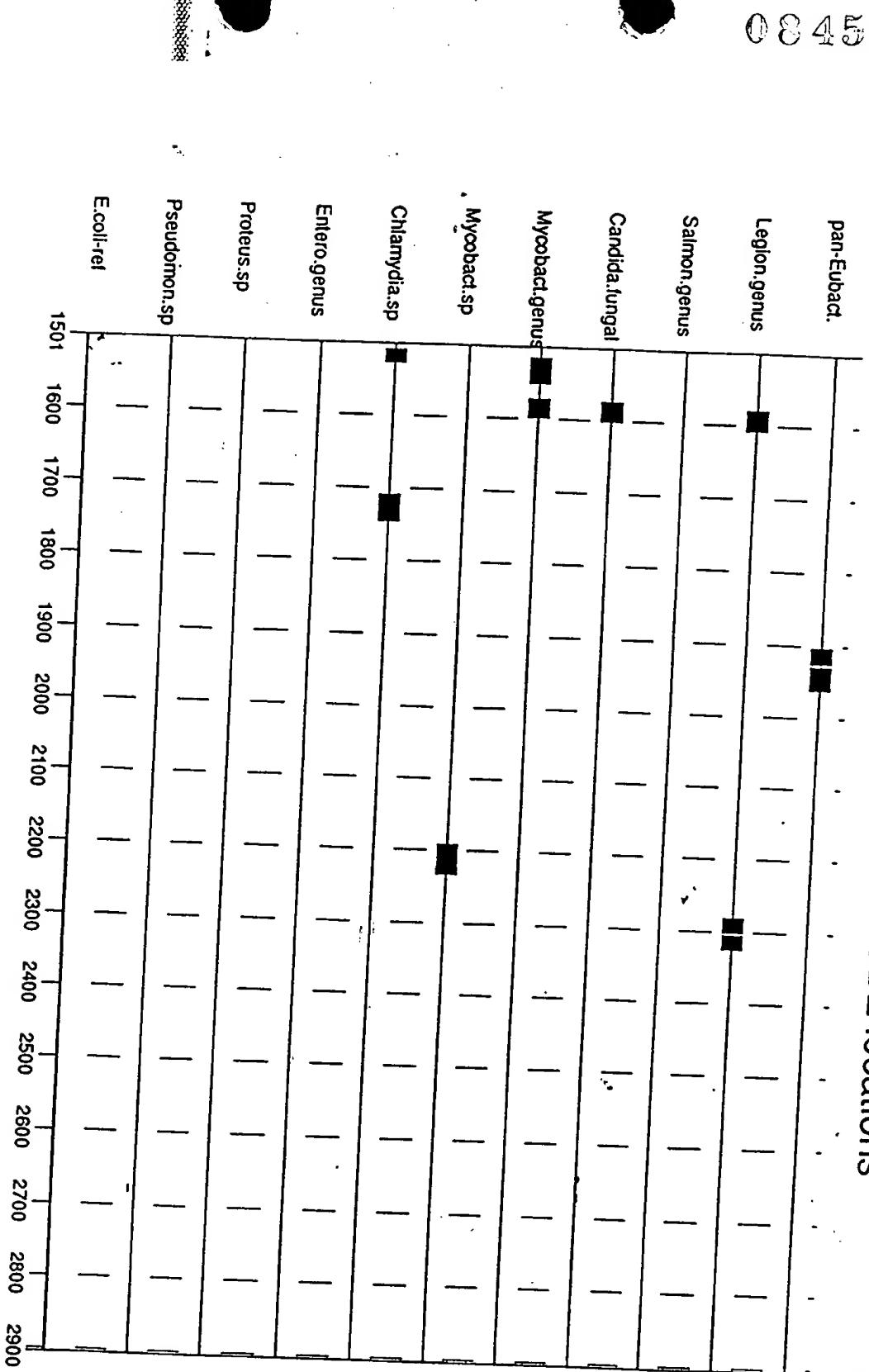


FIG. 11